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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/735,138
DATE: 01/04/2001
TIME: 09:31:42

Input Set : A:\TSRI548D1.txt
Output Set: N:\CRF3\01042001\I735138.raw

SEQUENCE LISTING

ENTERED

- 4 (1) GENERAL INFORMATION:
6 (i) APPLICANT: Sutcliffe, J. Gregor
7 Gautvik, Kaare M.
8 De Lecea, Luis
9 Bloom, Floyd E.
10 Danielson, Patria E.
11 Kilduff, T.S.
12 Gautvik, Vigdis T.
13 Foye, Pamela E.
15 (ii) TITLE OF INVENTION: Hypothalamus-Specific Polypeptides
17 (iii) NUMBER OF SEQUENCES: 15
19 (iv) CORRESPONDENCE ADDRESS:
20 (A) ADDRESSEE: Olson & Hierl, Ltd.
21 (B) STREET: 20 North Wacker Drive, 36th Floor
22 (C) CITY: Chicago
23 (D) STATE: IL
24 (E) COUNTRY: USA
25 (F) ZIP: 60606
27 (v) COMPUTER READABLE FORM:
28 (A) MEDIUM TYPE: Floppy disk
29 (B) COMPUTER: IBM PC compatible
30 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
31 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
33 (vi) CURRENT APPLICATION DATA:
34 (A) APPLICATION NUMBER: US/09/735,138
36 (B) FILING DATE: 12-Dec-2000
42 (C) CLASSIFICATION:
39 (vii) PRIOR APPLICATION DATA:
40 (A) APPLICATION NUMBER: 60/023,220
41 (B) FILING DATE: 02-AUG-1996
44 (viii) ATTORNEY/AGENT INFORMATION:
45 (A) NAME: Talivaldis Cepuritis
46 (B) REGISTRATION NUMBER: 20,818
47 (C) REFERENCE/DOCKET NUMBER: TSRI 548.1 DIV.1
49 (ix) TELECOMMUNICATION INFORMATION:
50 (A) TELEPHONE: 312-580-1180
51 (B) TELEFAX: 312-580-1189
54 (2) INFORMATION FOR SEQ ID NO: 1:
56 (i) SEQUENCE CHARACTERISTICS:
57 (A) LENGTH: 130 amino acids
58 (B) TYPE: amino acid
59 (C) STRANDEDNESS:
60 (D) TOPOLOGY: unknown
62 (ii) MOLECULE TYPE: protein
64 (iii) HYPOTHETICAL: NO
66 (iv) ANTI-SENSE: NO

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69 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
71 Met Asn Leu Pro Ser Thr Lys Val Pro Trp Ala Ala Val Thr Leu Leu
72 1 5 10 15
74 Leu Leu Leu Leu Leu Pro Pro Ala Leu Leu Ser Leu Gly Val Asp Ala
75 20 25 30
77 Gln Pro Leu Pro Asp Cys Cys Arg Gln Lys Thr Cys Ser Cys Arg Leu
78 35 40 45
80 Tyr Glu Leu Leu His Gly Ala Gly Asn His Ala Ala Gly Ile Leu Thr
81 50 55 60
83 Leu Gly Lys Arg Arg Pro Gly Pro Pro Gly Leu Gln Gly Arg Leu Gln
84 65 70 75 80
86 Arg Leu Leu Gln Ala Asn Gly Asn His Ala Ala Gly Ile Leu Thr Met
87 85 90 95
89 Gly Arg Arg Ala Gly Ala Glu Leu Glu Pro Tyr Pro Cys Pro Gly Arg
90 100 105 110
92 Arg Cys Pro Thr Ala Thr Ala Thr Ala Leu Ala Pro Arg Gly Gly Ser
93 115 120 125
95 Arg Val
96 130
99 (2) INFORMATION FOR SEQ ID NO: 2:
101 (i) SEQUENCE CHARACTERISTICS:
102 (A) LENGTH: 130 amino acids
103 (B) TYPE: amino acid
104 (C) STRANDEDNESS:
105 (D) TOPOLOGY: unknown
107 (ii) MOLECULE TYPE: protein
109 (iii) HYPOTHETICAL: NO
111 (iv) ANTI-SENSE: NO
114 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
116 Met Asn Phe Pro Ser Thr Lys Val Pro Trp Ala Ala Val Thr Leu Leu
117 1 5 10 15
119 Leu Leu Leu Leu Leu Pro Pro Ala Leu Leu Ser Leu Gly Val Asp Ala
120 20 25 30
122 Gln Pro Leu Pro Asp Cys Cys Arg Gln Lys Thr Cys Ser Cys Arg Leu
123 35 40 45
125 Tyr Glu Leu Leu His Gly Ala Gly Asn His Ala Ala Gly Ile Leu Thr
126 50 55 60
128 Leu Gly Lys Arg Arg Pro Gly Pro Pro Gly Leu Gln Gly Arg Leu Gln
129 65 70 75 80
131 Arg Leu Leu Gln Ala Asn Gly Asn His Ala Ala Gly Ile Leu Thr Met
132 85 90 95
134 Gly Arg Arg Ala Gly Ala Glu Leu Glu Pro His Pro Cys Ser Gly Arg
135 100 105 110
137 Gly Cys Pro Thr Val Thr Thr Thr Ala Leu Ala Pro Arg Gly Gly Ser
138 115 120 125
140 Gly Val
141 130
144 (2) INFORMATION FOR SEQ ID NO: 3:
146 (i) SEQUENCE CHARACTERISTICS:

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147      (A) LENGTH: 569 base pairs
148      (B) TYPE: nucleic acid
149      (C) STRANDEDNESS: single
150      (D) TOPOLOGY: unknown
152      (ii) MOLECULE TYPE: cDNA
154      (iii) HYPOTHETICAL: NO
156      (iv) ANTI-SENSE: NO
159      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
161      TAAGACGACG GCCTCAGACT CCTTGGGTAT TTGGACCACT GCACCGAAGA TACCATCTCT      60
163      CCGGATPACC TCTCCCTGAG CTCCAGACAC CATGAACCTT CCTTCTACAA AGGTTCCTCTG      120
165      GGCCGCCCTG ACGCTGCTGC TGCTGCTACT GCTGCCGCCG GCGCTGCTGT CGCTTGGGGT      180
167      GGACGCCGAG CCTCTGCCCG ACTGCTGTCTG CCAGAAGACG TGTTCCTGCC GGTCTACGA      240
169      ACTGTTGCAC GGAGCTGGCA ACCACGCCGC GGGCATCCTC ACTCTGGGAA AGCGGCGACC      300
171      TGGACCCCA GGCCTCCAAG GACGGCTGCA GCGCCTCCTT CAGGCCAAGC GTAACCACGC      360
173      AGCTGGCATC CTGACCATGG GCCGCCGCGC AGGCGCAGAG CTAGAGCCAT ATCCCTGCCC      420
175      TGGTCGCCGC TGTCGGACTG CAACCGCCAC CGCTTTAGCG CCCCGGGGCG GATCCAGAGT      480
177      CTGAACCCGT CTTCATATCC TGTCTAGTC CTAACCTTCC CCTCTCCTCG CCAGTCCCTA      540
179      GCAATAAAG ACGTTTCTCT GTTGGTGTG      569
182 (2) INFORMATION FOR SEQ ID NO: 4:
184      (i) SEQUENCE CHARACTERISTICS:
185          (A) LENGTH: 582 base pairs
186          (B) TYPE: nucleic acid
187          (C) STRANDEDNESS: single
188          (D) TOPOLOGY: linear
190      (ii) MOLECULE TYPE: cDNA
192      (iii) HYPOTHETICAL: NO
194      (iv) ANTI-SENSE: NO
196      (v) FRAGMENT TYPE: N-terminal
199      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
201      TAAGACGACG GCCTCAGACT TCTTGGGTAT TTGGACCACT GCACTGAAGA GATCATCTCT      60
203      CCAGATTAAT TTCCCTGAG CTCCAGGCAC CATGAACCTT CCTTCTACAA AGGTTCCTCTG      120
205      GGCCGCCCTG ACGCTGCTGC TGCTGCTACT GCTGCCACCG GCGCTGCTGT CGCTTGGGGT      180
207      GGACGCCAG CCTCTGCCCG ACTGCTGTCTG CCAGAAGACG TGTTCCTGCC GTCTCTACGA      240
209      ACTGTTGCAC GGAGCTGGCA ACCACGCTGC GGGTATCCTG ACTCTGGGAA AGCGGCGGCC      300
211      TGGACCTCCA GGCCTCCAGG GACGGCTGCA GCGCCTCCTT CAGGCCAAGC GTAACCACGC      360
213      AGCTGGCATC CTGACCATGG GCCGCCGCGC AGGCGCAGAG CTAGAGCCAC ATCCCTGCTC      420
215      TGGTCGCCGC TGTCGGACCG TAACTATCAC CGCTTTAGCA CCCCGGGGAG GGTCCGGAGT      480
217      TTGAACCCAT CTTCATCTCT TGTCTGATC CAAACTTCCC CCTCTGCTCG CCGCTGTCAG      540
219      TCTCTTGGTA AATGGCAATA AAGACGTTTC TCTGTGGTGT TG      582
222 (2) INFORMATION FOR SEQ ID NO: 5:
224      (i) SEQUENCE CHARACTERISTICS:
225          (A) LENGTH: 1458 base pairs
226          (B) TYPE: nucleic acid
227          (C) STRANDEDNESS: single
228          (D) TOPOLOGY: linear
230      (ii) MOLECULE TYPE: cDNA
232      (iii) HYPOTHETICAL: NO
234      (iv) ANTI-SENSE: NO
236      (v) FRAGMENT TYPE: N-terminal

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239 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
241 GCTAGGAGAC ATTGCGCGCG CGGTGGCGGC GTTGGCAGCA GCTGCAGACA TGCTGCTGCT 60
243 CAAGAAACAG ACGGAGGACA TCAGCAGTGT CTATGAGATC CGGGAGAAGC TGGGCTCGGG 120
245 TGCCTTCTCT GAGGTGATGC TGGCCAGGA AAGGGGCTCT GCTCATCTTG TGGCCCTCAA 180
247 GTGCATPCCC AAGAAAGCAC TCGGGGCAA GGAGGCCCTG GTGAGAAATG AGATCGCAGT 240
249 ACTCCGCAGG ATTAGCCACC CCAACATTGT GGCTCTGGAG GACGTCCACG AGAGCCCTTC 300
251 CCATCTCTAC TTGGCCATGG AGCTGGTAAC AGGTGGTGAA CTGTTTGACC GAATCATGGA 360
253 GCGGGGCTCC TACACAGAGA AGGATGCGAG CCACCTTGTA GGGCAGGTCC TTGGTGCTGT 420
255 CTCTACCTT CATAGCCTGG GCATCGTGCA CCGGGACCTC AAGCCTGAAA ACCTCCTCTA 480
257 TGCCACACCT TTTGAGGACT CCAAGATCAT GGTCTCTGAC TTTGGCCTGT CCAAAATTCA 540
259 AGCTGGCAAC ATGCTAGGCA CAGCCTGTGG GACCCAGGA TATGTGGCCC CAGAGCTCCT 600
261 GGAGCAGAAA CCGTACGGGA AGGCCGTAGA TGTGTGGGCC CTGGGTGTCA TCTCTACAT 660
263 CCGCTGTGT GGGTACCCCG CCTTCTATGA TGAGAGCGAT CCTGAACCTT TCAGCCAGAT 720
265 TCTGAGGGCC AGGTACGAGT TTGACTCTCC CTTTGGGAT GACATCTCAG AATCAGCCAA 780
267 AGACTTCATT CGGCACCTTC TGGACGTA TCCCCAGAAG AGGTTCACCT GCCACAGGC 840
269 CTTACAGCAT CTCGGATCT CTGGGATGC AGCCTTGGAC AGGACATCC TAGGTCTGT 900
271 CAGTGAGCAG ATCCAGAAGA ATTTGCCAG GACCCACTGG AAGCGTGCAT TCAATGCCAC 960
273 ATCATTCCTA CCTCACATCC GTAAGCTGGG ACAGAGCCCA GAGGCTGAGG AGGCTCCAG 1020
275 GCAGGGTATG ACCCGTCACA GCCACCCAGG CCTTGGGACT AGCCAGTCTC CCAAGTGGTG 1080
277 ACAACCAAGT GGATGCCAAG GAAGGCCAAG TGGACTGACT CCTAGCTTTT CTTTCTCCA 1140
279 GCCCTTTTGA TCTCCTCCC TGATCCTTGT CCCCCGACT GGCCTCTGTT GGAAAGTCCA 1200
281 AGACCGTGGG TGTATGCAT GGCCTGGGG TATGGGGCTT CCCAAGTATG TCCCAGCCT 1260
283 CTGTCTTTTG TTGCTGCCAC CCTCTATGGA AACTGAGGAG GTATTCAAAA ATGATTTGG 1320
285 GGGCCATCCT TCGTGACCT TGCAGCACA TATGCATTGC GTGGCTGTTT TGTCTTTGC 1380
287 TGAAGTGGG TGGTCTGCT TGTGTTGTAG CCCTTAGTCT CCTCTCTTT CCAACCAATA 1440
289 AAGACAAACA GAACAATG 1458
292 (2) INFORMATION FOR SEQ ID NO: 6:
294 (i) SEQUENCE CHARACTERISTICS:
295 (A) LENGTH: 103 amino acids
296 (B) TYPE: amino acid
297 (C) STRANDEDNESS:
298 (D) TOPOLOGY: unknown
300 (ii) MOLECULE TYPE: protein
302 (iii) HYPOTHETICAL: NO
304 (iv) ANTI-SENSE: NO
307 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
309 Leu Gly Val Asp Ala Gln Pro Leu Pro Asp Cys Cys Arg Gln Lys Thr
310 1 5 10 15
312 Cys Ser Cys Arg Leu Tyr Glu Leu Leu His Gly Ala Gly Asn His Ala
313 20 25 30
315 Ala Gly Ile Leu Thr Leu Gly Lys Arg Arg Pro Gly Pro Pro Gly Leu
316 35 40 45
318 Gln Gly Arg Leu Gln Arg Leu Leu Gln Ala Asn Gly Asn His Ala Ala
319 50 55 60
321 Gly Ile Leu Thr Met Gly Arg Arg Ala Gly Ala Glu Leu Glu Pro Tyr
322 65 70 75 80
324 Pro Cys Pro Gly Arg Arg Cys Pro Thr Ala Thr Ala Thr Ala Leu Ala
325 85 90 95
327 Pro Arg Gly Gly Ser Arg Val

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328                               100
331 (2) INFORMATION FOR SEQ ID NO: 7:
333   (i) SEQUENCE CHARACTERISTICS:
334       (A) LENGTH: 39 amino acids
335       (B) TYPE: amino acid
336       (C) STRANDEDNESS:
337       (D) TOPOLOGY: unknown
339   (ii) MOLECULE TYPE: protein
341   (iii) HYPOTHETICAL: NO
343   (iv) ANTI-SENSE: NO
346   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
348       Leu Gly Val Asp Ala Gln Pro Leu Pro Asp Cys Cys Arg Gln Lys Thr
349           1           5           10           15
351       Cys Ser Cys Arg Leu Tyr Glu Leu Leu His Gly Ala Gly Asn His Ala
352           20           25           30
354       Ala Gly Ile Leu Thr Leu Gly
355           35
358 (2) INFORMATION FOR SEQ ID NO: 8:
360   (i) SEQUENCE CHARACTERISTICS:
361       (A) LENGTH: 38 amino acids
362       (B) TYPE: amino acid
363       (C) STRANDEDNESS:
364       (D) TOPOLOGY: unknown
366   (ii) MOLECULE TYPE: protein
368   (iii) HYPOTHETICAL: NO
370   (iv) ANTI-SENSE: NO
373   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
375       Leu Gly Val Asp Ala Gln Pro Leu Pro Asp Cys Cys Arg Gln Lys Thr
376           1           5           10           15
377       Cys Ser Cys Arg Leu Tyr Glu Leu Leu His Gly Ala Gly Asn His Ala
378           20           25           30
379       Ala Gly Ile Leu Thr Leu
380           35
383 (2) INFORMATION FOR SEQ ID NO: 9:
385   (i) SEQUENCE CHARACTERISTICS:
386       (A) LENGTH: 28 amino acids
387       (B) TYPE: amino acid
388       (C) STRANDEDNESS:
389       (D) TOPOLOGY: unknown
391   (ii) MOLECULE TYPE: protein
393   (iii) HYPOTHETICAL: NO
395   (iv) ANTI-SENSE: NO
398   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
400       Pro Gly Pro Pro Gly Leu Gln Gly Arg Leu Gln Arg Leu Leu Gln Ala
401           1           5           10           15
403       Asn Gly Asn His Ala Ala Gly Ile Leu Thr Met Gly
404           20           25
407 (2) INFORMATION FOR SEQ ID NO: 10:
409   (i) SEQUENCE CHARACTERISTICS:

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/735,138

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L:34 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:36 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

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